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OM nucleic - nucleic search, using sw model

Run on: March 8, 2005, 05:37:07 ; Search time 474 Seconds
(without alignments)
9591.480 Million cell updates/sec

Title: US-09-939-537-32
Perfect score: 768
Sequence: 1 GCTAGCAGAGCCCAAATCTT.....GGGCTCTGGACGACGGATCC 768

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	768	100.0	768	2	AAT10780	Aat10780 Coding se
2	766.4	99.8	768	2	AAQ96101	Aaq96101 IgG1 hing
3	744.6	97.0	3143	13	ADR66793	Adr66793 Human pro
4	744.6	97.0	3143	13	ADR65890	Adr65890 Human pro
5	738.2	96.1	3075	13	ADR08053	Adr08053 Full leng
6	701	91.3	3183	13	ADR08303	Adr08303 Full leng
7	696	90.6	1827	8	ABT32045	Abt32045 Concatame
8	696	90.6	1827	12	ADQ79907	Adq79907 Human tum
9	695.2	90.5	7427	12	ADJ57518	Adj57518 Human FVI
10	695.2	90.5	7494	12	ADJ57515	Adj57515 Human FVI
11	695	90.5	1134	8	ABT32048	Abt32048 Concatame
12	695	90.5	1134	12	ADQ79913	Adq79913 Human CTL
13	695	90.5	1314	8	ABT32047	Abt32047 Concatame
14	695	90.5	1314	12	ADQ79911	Adq79911 Human CD2
15	695	90.5	1980	8	ABT32046	Abt32046 Concatame
16	695	90.5	1980	12	ADQ79909	Adq79909 Human tum
17	694.8	90.5	1104	12	ADF73151	Adf73151 RELP-Fc f
18	694.4	90.4	1335	8	ABT32041	Abt32041 Concatame
19	694.4	90.4	1335	12	ADQ79899	Adq79899 Human tum
20	694.4	90.4	1413	6	AAD45752	Aad45752 Human C2B
21	694.4	90.4	1413	8	ABZ24016	Abz24016 Antibody
22	694.4	90.4	1428	2	AAT61241	Aat61241 Human ant
23	694.4	90.4	1431	2	AAT62513	Aat62513 Primatise
24	694.4	90.4	1431	2	AAT62510	Aat62510 Primatise
25	694.4	90.4	1431	2	AAV35485	Aav35485 Macaque p
26	694.4	90.4	1431	2	AAV35489	Aav35489 Macaque p
27	694.4	90.4	1431	6	AAS17247	Aas17247 DNA seque
28	694.4	90.4	1431	6	AAS17243	Aas17243 DNA seque
29	694.4	90.4	1431	10	AAD56527	Aad56527 Monkey 7C
30	694.4	90.4	1437	2	AAV35487	Aav35487 Macaque p
31	694.4	90.4	1437	6	AAS17245	Aas17245 DNA seque
32	694.4	90.4	1437	10	AAD56529	Aad56529 Monkey 7B
33	694.4	90.4	1887	8	ABT32043	Abt32043 Concatame
34	694.4	90.4	1887	12	ADQ79903	Adq79903 Human tum
35	694.4	90.4	9209	9	ABX94203	Abx94203 TCAE8 exp
36	694.4	90.4	9209	10	ADE85693	Ade85693 Variable
37	694.4	90.4	9209	10	ACC78893	Acc78893 Chimeric
38	694.4	90.4	9209	12	ADN49730	Adn49730 Variable
39	693.8	90.3	1367	3	AAC67834	Aac67834 Fc-muAGP-
40	693.6	90.3	1173	6	ABA95203	Aba95203 MOG-Fc fu
41	693.6	90.3	1173	9	ADA14264	Ada14264 Human imm
42	693.4	90.3	705	12	ADL46173	Adl46173 Human imm
43	693.4	90.3	1473	8	ABT32042	Abt32042 Concatame
44	693.4	90.3	1473	12	ADQ79901	Adq79901 Human tum
45	693.4	90.3	2040	12	ADJ57517	Adj57517 Human FVI

ALIGNMENTS

RESULT 1
AAT10780
ID AAT10780 standard; DNA; 768 BP.
XX
AC AAT10780;
XX
DT 26-SEP-1996 (first entry)
XX
DE Coding sequence for IgG1 hinge, CH2 and CH3 domains.
XX
KW CD7; transmembrane domain; chimeric receptor; CD5; CD34; CH2; CH3; IgG1;
KW human; CD4; HIV; proteinaceous alpha-helix; T cell; B cell; neutrophil;
KW dendritic cell; therapy; mammal; infection; ss.
XX
OS Homo sapiens.
XX
PN WO9603883-A1.
XX
PD 15-FEB-1996.
XX
PF 26-JUL-1995; 95WO-US009468.
XX
PR 02-AUG-1994; 94US-00284391.
PR 24-FEB-1995; 95US-00394388.
XX
PA (GEHO) GEN HOSPITAL CORP.
XX
PI Seed B, Banapour B, Romeo C, Kolanus W;
XX
DR WPI; 1996-129034/13.
DR P-PSDB; AAR89441.
XX
PT Membrane-bound chimeric receptor comprising extracellular portion
PT including CD4 fragment - cells expressing receptor can be used for
PT treatment of HIV infection.
XX
PS Claim 3; Fig 25; 134pp; English.
XX
CC This sequence represents the coding sequence for the human IgG1 hinge,
CC CH2 and CH3 domains. This sequence is included in the membrane bound
CC proteinaceous chimeric receptor of the invention. Alternatively the
CC transmembrane region of the chimeric receptor contains a portion of the
CC CD7, CD5 or CD34 transmembrane domains. The extracellular portion of the

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CC   chimeric receptor contains a fragment of CD4 (amino acids 1-394 or 1-200
CC   of the CD4 sequence) which specifically recognises and binds HIV-infected
CC   cells, but does not mediate HIV infection. The extracellular domain of
CC   the receptor is separated from the cell membrane by 48 or 72 angstroms,
CC   or by one or more proteinaceous alpha-helices. The cells expressing the
CC   receptor are preferably T cells, B cells, neutrophils, or dendritic
CC   cells. The therapeutic cells expressing the chimeric receptor are
CC   administered to a mammal to treat HIV infection
XX
SQ   Sequence 768 BP; 186 A; 250 C; 213 G; 119 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 768;  DB 2;  Length 768;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-153;
  Matches  768;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCTAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GCTAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGA 60

Qy         61 ACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGAT 120

Qy        121 CTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGT 180

Qy        181 CAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGA 240

Qy        241 GGAGCAGTACAACAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GGAGCAGTACAACAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTG 300

Qy        301 GCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGA 360

Qy        361 GAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCC 420

Qy        421 ATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTA 480

Qy        481 TCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGAC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGAC 540

Qy        541 CACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGA 600

Qy        601 CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCA 660

Qy        661 CAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGGCTGCAACTGGACGAGACCTG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGGCTGCAACTGGACGAGACCTG 720

Qy        721 TGCTGAGGCCCAGGACGGGGAGCTGGACGGGCTCTGGACGACGGATCC 768
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGCTGAGGCCCAGGACGGGGAGCTGGACGGGCTCTGGACGACGGATCC 768


RESULT 2
AAQ96101
ID   AAQ96101 standard; DNA; 768 BP.
XX
AC   AAQ96101;
XX
DT   11-APR-1996  (first entry)
XX
DE   IgG1 hinge, CH2, CH3 domain-encoding DNA.
XX
KW   Chimeric receptor; CD4; T-cell receptor; HIV; cytolysis;
KW   human immunodeficiency virus; adoptive immunotherapy; IgG1; ss.
XX
OS   Homo sapiens.
XX
PN   WO9521528-A1.
XX
PD   17-AUG-1995.
XX
PF   12-JAN-1995;   95WO-US000454.
XX
PR   14-FEB-1994;   94US-00195395.
PR   02-AUG-1994;   94US-00284391.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
XX
PI   Seed B,  Banapour B,  Romeo C,  Kolanus W;
XX
DR   WPI; 1995-292893/38.
DR   P-PSDB; AAR78667.
XX
PT   Target cytolysis of HIV-infected cells - by chimeric CD4 receptor-bearing
PT   cells.
XX
PS   Disclosure; Fig 25; 118pp; English.
XX
CC   A DNA sequence coding for the hinge, CH2 and CH3 domains of human IgG1
CC   (AAR78667) is given in AAQ96101. It is used in the construction of a
CC   chimeric receptor utilised in the targeted cytolysis of HIV-infected
CC   cells. The chimeric receptor comprises the extracellular domain (pref.
CC   amino acids 1-394 or 1-200) of CD4 linked via the IgG1 hinge, CG2 and CD3
CC   domains to an intracellular portion, e.g. of T-cell receptor protein zeta
XX
SQ   Sequence 768 BP; 186 A; 249 C; 214 G; 119 T; 0 U; 0 Other;

  Query Match             99.8%;  Score 766.4;  DB 2;  Length 768;
  Best Local Similarity   99.9%;  Pred. No. 1.2e-152;
  Matches  767;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GCTAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GCTAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGA 60

Qy         61 ACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGAT 120

Qy        121 CTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGT 180

Qy        181 CAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGA 240

Qy        241 GGAGCAGTACAACAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GGAGCAGTACAACAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTG 300

Qy        301 GCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGA 360
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        301 GCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAAGAAAGCCCTCCCAGCCCCCATCGA 360

Qy        361 GAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCC 420

Qy        421 ATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTA 480
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTA 480

Qy        481 TCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGAC 540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGAC 540

Qy        541 CACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGA 600
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGA 600

Qy        601 CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCA 660
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCA 660

Qy        661 CAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGGCTGCAACTGGACGAGACCTG 720
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGGCTGCAACTGGACGAGACCTG 720

Qy        721 TGCTGAGGCCCAGGACGGGGAGCTGGACGGGCTCTGGACGACGGATCC 768
                ||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGCTGAGGCCCAGGACGGGGAGCTGGACGGGCTCTGGACGACGGATCC 768


RESULT 3
ADR66793
ID   ADR66793 standard; DNA; 3143 BP.
XX
AC   ADR66793;
XX
DT   02-DEC-2004  (first entry)
XX
DE   Human prostatic carcinoma derived DNA SEQ ID 86 #4.
XX
KW   human; cytostatic; diagnosis; prostatic cancer;
KW   differential expression analysis; ds.
XX
OS   Homo sapiens.
XX
PN   WO2004076614-A2.
XX
PD   10-SEP-2004.
XX
PF   22-FEB-2004; 2004WO-DE000433.
XX
PR   27-FEB-2003; 2003DE-01009985.
PR   14-MAY-2003; 2003DE-01022134.
XX
PA   (HINZ/) HINZMANN B.
PA   (DAHL/) DAHL E.
PA   (ROSE/) ROSENTHAL A.
PA   (HERM/) HERMANN K.
PA   (PILA/) PILARSKY C.
XX
PI   Hinzmann B,  Dahl E,  Rosenthal A,  Hermann K,  Pilarsky C,  Specht T;
PI   Schmitt A,  Beckmann G,  Bruemmendorf T,  Kinnemann H,  Roepcke S;
PI   Xinzhong L,  Staub E;
XX
DR   WPI; 2004-653386/63.
XX
PT   New nucleic acids, and encoded proteins, from prostatic cancer tissue,
PT   useful for diagnosis, treatment and in screening for specific binding
PT   agents.
XX
PS   Claim 1; Page 1464; 1607pp; German.
XX
CC   This invention describes novel cytostatic polynucleotide and polypeptide
CC   sequences which can be used in a method for diagnosing prostatic cancer
CC   or the risk of developing prostatic cancer. Diagnosis is based on
CC   determining over transcription or over expression of the sequences in
CC   prostatic tissue. Screening for inhibitors of the sequences or detection
CC   substances involves a binding assay, any compounds that bind are
CC   selected, optionally after deconvolution of mixtures. Detection of a
CC   predetermined minimum level of the reporter indicates the presence of
CC   tumour cells. Inhibitors can be chosen from antisense oligonucleotides,
CC   short-interfering RNA or ribozymes; an organic molecule of molecular
CC   weight below 5000, preferably 300, that binds to the polypeptide; an
CC   aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the
CC   polypeptide, preferably humanised or human; an anti-idiotype, non-human
CC   (monoclonal) antibody directed against Ab or any of the above derivatised
CC   with a reporter group, cell toxin, immunostimulatory molecules and/or
CC   radioisotope. The polynucleotides are identified in human prostatic
CC   cancer by differential expression analysis, using DNA microarrays,
CC   between normal and tumorous tissues, with (over)expression being detected
CC   by quantitative PCR. Analysis of prostatic cancer samples showed that
CC   CD24 was upregulated in many of them. Sections of tissue, isolated from
CC   prostatic cancer patients, or subjects at risk, were incubated
CC   sequentially with anti-human CD4 murine monoclonal antibodies;
CC   biotinylated second antibody; streptavidin-conjugated horseradish
CC   peroxidase and then diaminobenzidine as colour former (brown). The
CC   samples were counterstained with hemalum (blue). Malignant cells stained
CC   strongly but non-malignant cells only weakly. In 15 of 63 samples of
CC   adenocarcinoma, membrane and cytoplasmic staining was very strong, and
CC   lymph node metastases were also stained. ADR65805-ADR66954 represent the
CC   polynucleotide and polypeptide sequences used in the method of the
CC   invention.
XX
SQ   Sequence 3143 BP; 696 A; 993 C; 894 G; 560 T; 0 U; 0 Other;

  Query Match             97.0%;  Score 744.6;  DB 13;  Length 3143;
  Best Local Similarity   98.8%;  Pred. No. 5.9e-148;
  Matches  750;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          4 AGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACT 63
                ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        798 AGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACT 857

Qy         64 CCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTC 123
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        858 CCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTC 917

Qy        124 CCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAA 183
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        918 CCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAA 977

Qy        184 GTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGA 243
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        978 GTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGA 1037

Qy        244 GCAGTACAACAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCT 303
                |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db       1038 GCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCT 1097

Qy        304 GAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAA 363
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1098 GAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAA 1157

Qy        364 AACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATC 423
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1158 AACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATC 1217

Qy        424 CCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCC 483
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1218 CCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCC 1277

Qy        484 CAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCAC 543
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1278 CAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCAC 1337

Qy        544 GCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAA 603
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1338 GCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAA 1397

Qy        604 GAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAA 663
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1398 GAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAA 1457
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Qy        664 CCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGGCTGCAACTGGACGAGACCTGTGC 723
              ||||||||||||||||||||||||||||||||||| |||||||||||| |||| ||||||
Db       1458 CCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGAGCTGCAACTGGAGGAGAGCTGTGC 1517

Qy        724 TGAGGCCCAGGACGGGGAGCTGGACGGGCTCTGGACGAC 762
              ||||| |||||||||||||||||||||||| ||||||||
Db       1518 GGAGGCGCAGGACGGGGAGCTGGACGGGCTGTGGACGAC 1556
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RESULT 4
ADR65890
ID ADR65890 standard; DNA; 3143 BP.
XX
AC ADR65890;
XX
DT 02-DEC-2004 (first entry)
XX
DE Human prostatic carcinoma derived DNA SEQ ID 86 #1.
XX
KW human; cytostatic; diagnosis; prostatic cancer;
KW differential expression analysis; ds.
XX
OS Homo sapiens.
XX
PN WO2004076614-A2.
XX
PD 10-SEP-2004.
XX
PF 22-FEB-2004; 2004WO-DE000433.
XX
PR 27-FEB-2003; 2003DE-01009985.
PR 14-MAY-2003; 2003DE-01022134.
XX
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
XX
PI Hinzmann B, Dahl E, Rosenthal A, Hermann K, Pilarsky C, Specht T;
PI Schmitt A, Beckmann G, Bruemmendorf T, Kinnemann H, Roepcke S;
PI Xinzhong L, Staub E;
XX
DR WPI; 2004-653386/63.
XX
PT New nucleic acids, and encoded proteins, from prostatic cancer tissue,
PT useful for diagnosis, treatment and in screening for specific binding
PT agents.
XX
PS Claim 1; Page 294; 1607pp; German.
XX
CC This invention describes novel cytostatic polynucleotide and polypeptide
CC sequences which can be used in a method for diagnosing prostatic cancer
CC or the risk of developing prostatic cancer. Diagnosis is based on
CC determining over transcription or over expression of the sequences in
CC prostatic tissue. Screening for inhibitors of the sequences or detection
CC substances involves a binding assay, any compounds that bind are
CC selected, optionally after deconvolution of mixtures. Detection of a
CC predetermined minimum level of the reporter indicates the presence of
CC tumour cells. Inhibitors can be chosen from antisense oligonucleotides,
CC short-interfering RNA or ribozymes; an organic molecule of molecular
CC weight below 5000, preferably 300, that binds to the polypeptide; an
CC aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the
CC polypeptide, preferably humanised or human; an anti-idiotype, non-human
CC (monoclonal) antibody directed against Ab or any of the above derivatised
CC with a reporter group, cell toxin, immunostimulatory molecules and/or
CC radioisotope. The polynucleotides are identified in human prostatic
CC cancer by differential expression analysis, using DNA microarrays,
CC between normal and tumorous tissues, with (over)expression being detected
CC by quantitative PCR. Analysis of prostatic cancer samples showed that
CC CD24 was upregulated in many of them. Sections of tissue, isolated from
CC prostatic cancer patients, or subjects at risk, were incubated
CC sequentially with anti-human CD4 murine monoclonal antibodies;
CC biotinylated second antibody; streptavidin-conjugated horseradish
CC peroxidase and then diaminobenzidine as colour former (brown). The
CC samples were counterstained with hemalum (blue). Malignant cells stained
CC strongly but non-malignant cells only weakly. In 15 of 63 samples of
CC adenocarcinoma, membrane and cytoplasmic staining was very strong, and
CC lymph node metastases were also stained. ADR65805-ADR66954 represent the
CC polynucleotide and polypeptide sequences used in the method of the
CC invention.
XX
SQ Sequence 3143 BP; 696 A; 993 C; 894 G; 560 T; 0 U; 0 Other;

Query Match 97.0%; Score 744.6; DB 13; Length 3143;
Best Local Similarity 98.8%; Pred. No. 5.9e-148;
Matches 750; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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Qy          4 AGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACT 63
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        798 AGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACT 857

Qy         64 CCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTC 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        858 CCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTC 917

Qy        124 CCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAA 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        918 CCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAA 977

Qy        184 GTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGA 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        978 GTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGA 1037

Qy        244 GCAGTACAACAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCT 303
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db       1038 GCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCT 1097

Qy        304 GAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAA 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1098 GAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAA 1157

Qy        364 AACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATC 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1158 AACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATC 1217

Qy        424 CCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCC 483
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1218 CCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCC 1277

Qy        484 CAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCAC 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1278 CAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCAC 1337

Qy        544 GCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAA 603
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1338 GCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAA 1397

Qy        604 GAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAA 663
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1398 GAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAA 1457

Qy        664 CCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGGCTGCAACTGGACGAGACCTGTGC 723
              ||||||||||||||||||||||||||||||||||| |||||||||||| |||| ||||||
Db       1458 CCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGAGCTGCAACTGGAGGAGAGCTGTGC 1517

Qy        724 TGAGGCCCAGGACGGGGAGCTGGACGGGCTCTGGACGAC 762
              ||||| |||||||||||||||||||||||| ||||||||
Db       1518 GGAGGCGCAGGACGGGGAGCTGGACGGGCTGTGGACGAC 1556
```

RESULT 5
ADR08053
ID ADR08053 standard; cDNA; 3075 BP.
XX

```
AC   ADR08053;
XX
DT   04-NOV-2004  (first entry)
XX
DE   Full length human cDNA useful for treating neurological disease Seq 1559.
XX
KW   gene; ss; human; oligo-capping method; diagnostic marker; gene therapy;
KW   osteoporosis; neurological disease; Alzheimer's disease;
KW   Parkinson's disease; dementia; short memory; cancer;
KW   sense or motor function; emotional reaction; fear response; panic;
KW   osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;
KW   tranquiliser.
XX
OS   Homo sapiens.
XX
PN   EP1447413-A2.
XX
PD   18-AUG-2004.
XX
PF   12-FEB-2004; 2004EP-00003145.
XX
PR   14-FEB-2003; 2003JP-00102207.
PR   09-MAY-2003; 2003JP-00131452.
XX
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI   Isogai T,  Yamamoto J,  Nishikawa T,  Isono Y,  Sugiyama T,  Otsuki T;
PI   Wakamatsu A,  Ishii S,  Nagai K,  Irie R;
XX
DR   WPI; 2004-583265/57.
DR   P-PSDB; ADR10009.
XX
PT   New 1995 cDNA, useful for treating osteoporosis, neurological diseases,
PT   Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
XX
PS   Claim 1; SEQ ID NO 1559; 2686pp; English.
XX
CC   This invention relates to novel, isolated full length human cDNA
CC   molecules and the encoded proteins thereof. Specifically, it refers to
CC   cDNA clones obtained by an oligo-capping method, where none of these
CC   clones are identical to any known human mRNAs. The present invention
CC   describes an immunoassay to identify agonists and antagonists, as well as
CC   antibodies, antisense molecules and siRNAs that can all be used to bind
CC   to and modulate expression of the cDNA molecules. As such, these
CC   molecules are useful for diagnostic markers or therapeutic targets for
CC   the various diseases or morbid states. In particular, they are useful in
CC   gene therapy for treating osteoporosis, neurological disease, Alzheimer's
CC   disease, Parkinson's disease, dementia, short memory and various cancers,
CC   as well as for maintaining equilibrium of sense or motor function, and
CC   for treating emotional reaction, fear response and panic. Accordingly,
CC   they exhibit osteopathic, neuroprotective, nootropic, antiparkinsonian,
CC   cytostatic and tranquiliser activities. This polynucleotide is a full
CC   length human cDNA sequence of the invention. NOTE: This sequence is not
CC   given in the sequence listing of the specification but can be obtained on
CC   CD-ROM from the European Patent Office, Vienna Sub-office.
XX
SQ   Sequence 3075 BP; 666 A; 972 C; 887 G; 550 T; 0 U; 0 Other;

  Query Match             96.1%;  Score 738.2;  DB 13;  Length 3075;
  Best Local Similarity   98.3%;  Pred. No. 1.3e-146;
  Matches  746;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          4 AGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACT 63
              ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        748 AGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACT 807

Qy         64 CCTGGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTC 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        808 CCTGGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTC 867

Qy        124 CCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAA 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        868 CCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAA 927

Qy        184 GTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGA 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        928 GTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGA 987

Qy        244 GCAGTACAACAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCT 303
              ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        988 GCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCT 1047

Qy        304 GAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAA 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1048 GAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAA 1107

Qy        364 AACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATC 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1108 AACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATC 1167

Qy        424 CCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCC 483
              |||||| ||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db       1168 CCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCC 1227

Qy        484 CAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCAC 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1228 CAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCAC 1287

Qy        544 GCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAA 603
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db       1288 GCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAA 1347

Qy        604 GAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAA 663
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1348 GAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAA 1407

Qy        664 CCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGGCTGCAACTGGACGAGACCTGTGC 723
              |||||||||||||||||||||||||||||| |||| |||||||||||| |||| ||||||
Db       1408 CCACTACACGCAGAAGAGCCTCTCCCTGTCCCCGGAGCTGCAACTGGAGGAGAGCTGTGC 1467

Qy        724 TGAGGCCCAGGACGGGGAGCTGGACGGGCTCTGGACGAC 762
                |||| |||||||||||||||||||||||| ||||||||
Db       1468 GGAGGCGCAGGACGGGGAGCTGGACGGGCTGTGGACGAC 1506


RESULT 6
ADR08303
ID   ADR08303 standard; cDNA; 3183 BP.
XX
AC   ADR08303;
XX
DT   04-NOV-2004  (first entry)
XX
DE   Full length human cDNA useful for treating neurological disease Seq 1809.
XX
KW   gene; ss; human; oligo-capping method; diagnostic marker; gene therapy;
KW   osteoporosis; neurological disease; Alzheimer's disease;
KW   Parkinson's disease; dementia; short memory; cancer;
KW   sense or motor function; emotional reaction; fear response; panic;
KW   osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;
KW   tranquiliser.
XX
OS   Homo sapiens.
XX
PN   EP1447413-A2.
XX
PD   18-AUG-2004.
XX
PF   12-FEB-2004; 2004EP-00003145.
XX
PR   14-FEB-2003; 2003JP-00102207.
PR   09-MAY-2003; 2003JP-00131452.
XX
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI   Isogai T,  Yamamoto J,  Nishikawa T,  Isono Y,  Sugiyama T,  Otsuki T;
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PI Wakamatsu A, Ishii S, Nagai K, Irie R;
XX
DR WPI; 2004-583265/57.
DR P-PSDB; ADR10259.
XX
PT New 1995 cDNA, useful for treating osteoporosis, neurological diseases,
PT Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
XX
PS Claim 1; SEQ ID NO 1809; 2686pp; English.
XX
CC This invention relates to novel, isolated full length human cDNA
CC molecules and the encoded proteins thereof. Specifically, it refers to
CC cDNA clones obtained by an oligo-capping method, where none of these
CC clones are identical to any known human mRNAs. The present invention
CC describes an immunoassay to identify agonists and antagonists, as well as
CC antibodies, antisense molecules and siRNAs that can all be used to bind
CC to and modulate expression of the cDNA molecules. As such, these
CC molecules are useful for diagnostic markers or therapeutic targets for
CC the various diseases or morbid states. In particular, they are useful in
CC gene therapy for treating osteoporosis, neurological disease, Alzheimer's
CC disease, Parkinson's disease, dementia, short memory and various cancers,
CC as well as for maintaining equilibrium of sense or motor function, and
CC for treating emotional reaction, fear response and panic. Accordingly,
CC they exhibit osteopathic, neuroprotective, nootropic, antiparkinsonian,
CC cytostatic and tranquiliser activities. This polynucleotide is a full
CC length human cDNA sequence of the invention. NOTE: This sequence is not
CC given in the sequence listing of the specification but can be obtained on
CC CD-ROM from the European Patent Office, Vienna Sub-office.
XX
SQ Sequence 3183 BP; 685 A; 1025 C; 889 G; 584 T; 0 U; 0 Other;

Query Match 91.3%; Score 701; DB 13; Length 3183;
Best Local Similarity 95.4%; Pred. No. 9.8e-139;
Matches 722; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

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Qy          6 CAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 65
              |||||||||||||||||||| | ||| | ||||||||| ||||||||||||||||||||
Db        866 CAGAGCCCAAATCTTGTGACACACCTCCCCCATGCCCACGGTGCCCAGCACCTGAACTCC 925

Qy         66 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 125
              |||| ||||||||||||||||||||||||||||||||||||||| ||||| ||||| ||||
Db        926 TGGGAGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGATACCCTTATGATTTCCC 985

Qy        126 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 185
              |||||||||||||||| |||||||||||||||||||||||||||||||| ||||||| |||
Db        986 GGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCCGAGGTCCAGT 1045

Qy        186 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 245
              |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1046 TCAAGTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 1105

Qy        246 AGTACAACAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 305
              ||| |||||||||||| ||| ||||||||||||||||||||||||||||||||||||||||
Db       1106 AGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 1165

Qy        306 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 365
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1166 ACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 1225

Qy        366 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 425
              |||||||||| ||||||| ||||||||||||||||||||||||||||||||||||||||||
Db       1226 CCATCTCCAAAACCAAAGGACAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 1285

Qy        426 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 485
              |||| ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1286 GGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCA 1345

Qy        486 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 545
              |||||||||||||||||||||||||||  |||||||||||||||||||||| |||||||
Db       1346 GCGACATCGCCGTGGAGTGGGAGAGCAGCGGGCAGCCGGAGAACAACTACAACACCACGC 1405

Qy        546 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 605
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1406 CTCCCATGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 1465

Qy        606 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 665
              |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db       1466 GCAGGTGGCAGCAGGGGAACATCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 1525

Qy        666 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGGCTGCAACTGGACGAGACCTGTGCTG 725
              || |||||||||||||||||||||||||||||| |||||||||||| |||| |||||| |
Db       1526 GCTTCACGCAGAAGAGCCTCTCCCTGTCTCCGGAGCTGCAACTGGAGGAGAGCTGTGCGG 1585

Qy        726 AGGCCCAGGACGGGGAGCTGGACGGGCTCTGGACGAC 762
              |||| |||||||||||||||||||||| ||||||||
Db       1586 AGGCGCAGGACGGGGAGCTGGACGGGCTGTGGACGAC 1622
```

RESULT 7
ABT32045
ID ABT32045 standard; DNA; 1827 BP.
XX
AC ABT32045;
XX
DT 08-MAY-2003 (first entry)
XX
DE Concatameric immunoadhesion human DNA sequence SEQ ID No 9.
XX
KW Antiinflammatory; antibacterial; immunosuppressive; antirheumatic;
KW antiarthritic; immunomodulator; concatameric protein; soluble domain;
KW dimeric protein; inflammation; septicaemia; cytotoxicity;
KW rheumatoid arthritis; cachexia; inflammation; human; gene; ds.
XX
OS Homo sapiens.
XX
PN WO2003010202-A1.
XX
PD 06-FEB-2003.
XX
PF 26-JUL-2002; 2002WO-KR001427.
XX
PR 26-JUL-2001; 2001KR-00045028.
XX
PA (MEDE-) MEDEXGEN CO LTD.
XX
PI Chung Y, Han J, Lee H, Choi E, Kim J;
XX
DR WPI; 2003-229639/22.
DR P-PSDB; ABJ37102.
XX
PT New concatameric protein having two soluble domains, useful for
PT diagnosing and treating disorders associated with the dimeric protein or
PT its glycosylated form, such as inflammation, septicemia, rheumatoid
PT arthritis and cachexia.
XX
PS Claim 29; Page 135-139; 211pp; English.
XX
CC The invention relates to a novel concatameric protein comprising two
CC soluble domains, in which an N-terminus of a soluble domain of a
CC biologically active protein is linked to a C-terminus of an identical
CC soluble domain or a different soluble domain of a biologically active
CC protein. The methods and compositions of the present invention are useful
CC for the diagnosis and treatment of disorders associated with dimeric
CC protein or its glycosylated form, such as inflammation, septicaemia,
CC cytotoxicity, rheumatoid arthritis, cachexia and other inflammation-
CC related diseases. This polynucleotide sequence represents the DNA
CC encoding a human concatameric protein of the invention
XX
SQ Sequence 1827 BP; 474 A; 524 C; 481 G; 348 T; 0 U; 0 Other;

Query Match 90.6%; Score 696; DB 8; Length 1827;
Best Local Similarity 100.0%; Pred. No. 1e-137;
Matches 696; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          4 AGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACT 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1125 AGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACT 1184

Qy         64 CCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTC 123
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1185 CCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTC 1244

Qy        124 CCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAA 183
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1245 CCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAA 1304

Qy        184 GTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGA 243
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1305 GTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGA 1364

Qy        244 GCAGTACAACAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCT 303
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1365 GCAGTACAACAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCT 1424

Qy        304 GAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAA 363
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1425 GAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAA 1484

Qy        364 AACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATC 423
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1485 AACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATC 1544

Qy        424 CCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCC 483
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1545 CCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCC 1604

Qy        484 CAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCAC 543
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1605 CAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCAC 1664

Qy        544 GCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAA 603
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1665 GCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAA 1724

Qy        604 GAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAA 663
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1725 GAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAA 1784

Qy        664 CCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG 699
              |||||||||||||||||||||||||||||||||||
Db       1785 CCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG 1820


RESULT 8
ADQ79907
ID   ADQ79907 standard; DNA; 1827 BP.
XX
AC   ADQ79907;
XX
DT   09-SEP-2004  (first entry)
XX
DE   Human tumour necrosis factor receptor 1, mgTNFR1-TNFR1/Ig construct, DNA.
XX
KW   Human; tumour necrosis factor receptor; TNFR1; TNFR2; CTLA4; CD2; IgG;
KW   immunoglobulin; ds; concatameric fused dimer protein; immunoadhesin;
KW   Fc fragment; hinge.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   KR2004009997-A.
XX
PD   31-JAN-2004.
XX
PF   26-JUL-2002; 2002KR-00045921.
XX
PR   26-JUL-2002; 2002KR-00045921.
XX
PA   (MEDE-) MEDEXGEN INC.
XX
PI   Choi EY,  Han JU,  Jung YH,  Kim JM,  Lee HJ;
XX
DR   WPI; 2004-458871/43.
DR   P-PSDB; ADQ79908.
XX
PT   Concatameric immunoadhesin.
XX
PS   Claim 29; SEQ ID NO 9; 129pp; Korean.
XX
CC   The invention relates to a concatameric fused dimer protein and
CC   glycosylation modification protein providing concatameric immunoadhesin
CC   with improved efficacy and stability. The concatameric protein is
CC   characteristically formed by binding C-terminal of one biologically
CC   active protein with N-terminal of same or different biologically active
CC   protein, e.g. tumour necrosis factor receptors (TNFR1 and TNFR2), CD2 and
CC   CTLA4. Two monomer proteins which are formed by fusing the extracellular
CC   region of a protein participating in the same immune reaction to an
CC   immunoglobulin Fc fragment, bound together at a hinge region by
CC   disulphide bond to give the concatameric fused dimer protein, wherein the
CC   immunoglobulin is IgG. The present sequence encodes a monomeric or
CC   dimeric IgG fusion protein (or a dimeric fusion protein containing
CC   engineered N-glycosylation sites, designated "mg").
XX
SQ   Sequence 1827 BP; 474 A; 524 C; 481 G; 348 T; 0 U; 0 Other;

  Query Match            90.6%;  Score 696;  DB 12;  Length 1827;
  Best Local Similarity  100.0%;  Pred. No. 1e-137;
  Matches  696;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 AGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACT 63
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1125 AGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACT 1184

Qy         64 CCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTC 123
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1185 CCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTC 1244

Qy        124 CCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAA 183
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1245 CCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAA 1304

Qy        184 GTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGA 243
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1305 GTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGA 1364

Qy        244 GCAGTACAACAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCT 303
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1365 GCAGTACAACAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCT 1424

Qy        304 GAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAA 363
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1425 GAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAA 1484

Qy        364 AACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATC 423
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1485 AACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATC 1544

Qy        424 CCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCC 483
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1545 CCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCC 1604

Qy        484 CAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCAC 543
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1605 CAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCAC 1664

Qy        544 GCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAA 603
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1665 GCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAA 1724

Qy        604 GAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAA 663
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1725 GAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAA 1784
```

```
Qy        664 CCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG 699
              |||||||||||||||||||||||||||||||||||
Db       1785 CCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG 1820


RESULT 9
ADJ57518
ID   ADJ57518 standard; cDNA; 7427 BP.
XX
AC   ADJ57518;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Human FVII-IgG1 Fc domain fusion protein encoding cDNA.
XX
KW   TF; tissue factor; FVIIa; factor VII; anticoagulant; thrombolytic;
KW   cerebroprotective; cytostatic; vasotropic; antirheumatic; antiarthritic;
KW   antiarteriosclerotic; antiinflammatory; antibacterial; immunosuppressive;
KW   hypertensive; cardiant; human; coagulation Factor VII; immunoglobulin G1;
KW   IgG1; fusion protein; gene; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             11. .2050
FT                   /*tag= a
FT                   /product= "FVII-IgG1 fc domain"
FT                   /transl_except= (pos:1145. .1147, aa: Lys)
XX
PN   WO2004006962-A2.
XX
PD   22-JAN-2004.
XX
PF   09-JUL-2003; 2003WO-DK000481.
XX
PR   12-JUL-2002; 2002DK-00001099.
XX
PA   (NOVO ) NOVO NORDISK AS.
XX
PI   Bjorn SE,  Nicolaisen EM,  Steenstrup TD;
XX
DR   WPI; 2004-180224/17.
DR   P-PSDB; ADJ57516.
XX
PT   New compound binding to tissue factor, useful for treating diseases such
PT   as angiogenesis, ischemia/reperfusion, and rheumatoid arthritis.
XX
PS   Disclosure; SEQ ID NO 13; 61pp; English.
XX
CC   The invention relates to a compound (I) binding to tissue factor (TF).
CC   The compound (I) has the formula A-(LM)-C, where A is a FVIIa
CC   polypeptide, LM is an optional linker group, C comprises an
CC   immunostimulatory effector domain, and (I) binds to TF. (I) inhibits TF-
CC   mediated activated factor VII (FVIIa) activity. (I) is useful as a
CC   medicament, and for the manufacture of a medicament for preventing or
CC   treating disease or disorder associated with pathophysiological TF
CC   activity. The disease or disorder associated with pathophysiological TF
CC   activity are deep venous thrombosis, arterial thrombosis, post surgical
CC   thrombosis, coronary artery bypass graft (CABG), percutaneous transdermal
CC   coronary angioplastry (PTCA), stroke, cancer, tumor metastasis,
CC   angiogenesis, ischemia/reperfusion, rheumatoid arthritis, thrombolysis,
CC   arteriosclerosis and restenosis following angioplastry, acute and chronic
CC   indications such as inflammation, septic shock, septicemia, hypotension,
CC   adult respiratory distress syndrome (ARDS), disseminated intravascular
CC   coagulopathy (DIC), pulmonary embolism, platelet deposition, myocardial
CC   infarction, or prophylactic treatment of mammals with atherosclerotic
CC   vessels at risk for thrombosis. The present sequence represents the
CC   nucleotide sequence of a vector comprising the cDNA encoding the native
CC   human coagulation Factor VII with alternative spliced propetide
CC   conjugated to Fc domain of immunoglobulin G1 (IgG1)
XX
SQ   Sequence 7427 BP; 1678 A; 2042 C; 1988 G; 1719 T; 0 U; 0 Other;

  Query Match             90.5%;  Score 695.2;  DB 12;  Length 7427;
  Best Local Similarity   98.2%;  Pred. No. 1.8e-137;
  Matches  703;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          5 GCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTC 64
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1349 GCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTC 1408

Qy         65 CTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCC 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1409 CTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCC 1468

Qy        125 CGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAG 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1469 CGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAG 1528

Qy        185 TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAG 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1529 TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAG 1588

Qy        245 CAGTACAACAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG 304
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db       1589 CAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG 1648

Qy        305 AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAA 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1649 AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAA 1708

Qy        365 ACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCC 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1709 ACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCC 1768

Qy        425 CGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1769 CGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC 1828

Qy        485 AGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACG 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1829 AGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACG 1888

Qy        545 CCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAG 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1889 CCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAG 1948

Qy        605 AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAC 664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1949 AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAC 2008

Qy        665 CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGGCTGCAACTGGACGAGACCTG 720
              ||||||||||||||||||||||||||||||||||      | || |||   |||
Db       2009 CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGAAAGGGCGAATTCTG 2064


RESULT 10
ADJ57515
ID   ADJ57515 standard; cDNA; 7494 BP.
XX
AC   ADJ57515;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Human FVII-IgG1 Fc domain fusion protein-encoding cDNA.
XX
KW   TF; tissue factor; FVIIa; factor VII; anticoagulant; thrombolytic;
KW   cerebroprotective; cytostatic; vasotropic; antirheumatic; antiarthritic;
KW   antiarteriosclerotic; antiinflammatory; antibacterial; immunosuppressive;
KW   hypertensive; cardiant; human; coagulation Factor VII; immunoglobulin G1;
KW   IgG1; fusion protein; gene; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
```

```
XX
FH   Key             Location/Qualifiers
FT   CDS             11. .2106
FT                   /*tag=  a
FT                   /product= "FVII-IgG1 fc domain"
FT                   /transl_except= (pos:1211. .1213, aa: Lys)
XX
PN   WO2004006962-A2.
XX
PD   22-JAN-2004.
XX
PF   09-JUL-2003; 2003WO-DK000481.
XX
PR   12-JUL-2002; 2002DK-00001099.
XX
PA   (NOVO ) NOVO NORDISK AS.
XX
PI   Bjorn SE,  Nicolaisen EM,  Steenstrup TD;
XX
DR   WPI; 2004-180224/17.
DR   P-PSDB; ADJ57511.
XX
PT   New compound binding to tissue factor, useful for treating diseases such
PT   as angiogenesis, ischemia/reperfusion, and rheumatoid arthritis.
XX
PS   Disclosure; SEQ ID NO 10; 61pp; English.
XX
CC   The invention relates to a compound (I) binding to tissue factor (TF).
CC   The compound (I) has the formula A-(LM)-C, where A is a FVIIa
CC   polypeptide, LM is an optional linker group, C comprises an
CC   immunostimulatory effector domain, and (I) binds to TF. (I) inhibits TF-
CC   mediated activated factor VII (FVIIa) activity. (I) is useful as a
CC   medicament, and for the manufacture of a medicament for preventing or
CC   treating disease or disorder associated with pathophysiological TF
CC   activity. The disease or disorder associated with pathophysiological TF
CC   activity are deep venous thrombosis, arterial thrombosis, post surgical
CC   thrombosis, coronary artery bypass graft (CABG), percutaneous transdermal
CC   coronary angioplastry (PTCA), stroke, cancer, tumor metastasis,
CC   angiogenesis, ischemia/reperfusion, rheumatoid arthritis, thrombolysis,
CC   arteriosclerosis and restenosis following angioplastry, acute and chronic
CC   indications such as inflammation, septic shock, septicemia, hypotension,
CC   adult respiratory distress syndrome (ARDS), disseminated intravascular
CC   coagulopathy (DIC), pulmonary embolism, platelet deposition, myocardial
CC   infarction, or prophylactic treatment of mammals with atherosclerotic
CC   vessels at risk for thrombosis. The present sequence represents the
CC   nucleotide sequence of a vector comprising the cDNA encoding the native
CC   human coagulation Factor VII with alternative spliced propetide
CC   conjugated to Fc domain of immunoglobulin G1 (IgG1)
XX
SQ   Sequence 7494 BP; 1694 A; 2063 C; 2013 G; 1724 T; 0 U; 0 Other;

  Query Match             90.5%;  Score 695.2;  DB 12;  Length 7494;
  Best Local Similarity   98.2%;  Pred. No. 1.8e-137;
  Matches  703;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          5 GCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTC 64
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1415 GCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTC 1474

Qy         65 CTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCC 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1475 CTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCC 1534

Qy        125 CGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAG 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1535 CGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAG 1594

Qy        185 TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAG 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1595 TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAG 1654

Qy        245 CAGTACAACAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG 304
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db       1655 CAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG 1714

Qy        305 AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAA 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1715 AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAA 1774

Qy        365 ACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCC 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1775 ACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCC 1834

Qy        425 CGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1835 CGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC 1894

Qy        485 AGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACG 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1895 AGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACG 1954

Qy        545 CCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAG 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1955 CCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAG 2014

Qy        605 AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAC 664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2015 AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAC 2074

Qy        665 CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGGCTGCAACTGGACGAGACCTG 720
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2075 CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGAAAGGGCGAATTCTG 2130


RESULT 11
ABT32048
ID   ABT32048 standard; DNA; 1134 BP.
XX
AC   ABT32048;
XX
DT   08-MAY-2003  (first entry)
XX
DE   Concatameric immunoadhesion human DNA sequence SEQ ID No 15.
XX
KW   Antiinflammatory; antibacterial; immunosuppressive; antirheumatic;
KW   antiarthritic; immunomodulator; concatameric protein; soluble domain;
KW   dimeric protein; inflammation; septicaemia; cytotoxicity;
KW   rheumatoid arthritis; cachexia; inflammation; human; gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO2003010202-A1.
XX
PD   06-FEB-2003.
XX
PF   26-JUL-2002; 2002WO-KR001427.
XX
PR   26-JUL-2001; 2001KR-00045028.
XX
PA   (MEDE-) MEDEXGEN CO LTD.
XX
PI   Chung Y,  Han J,  Lee H,  Choi E,  Kim J;
XX
DR   WPI; 2003-229639/22.
DR   P-PSDB; ABJ37105.
XX
PT   New concatameric protein having two soluble domains, useful for
PT   diagnosing and treating disorders associated with the dimeric protein or
PT   its glycosylated form, such as inflammation, septicemia, rheumatoid
PT   arthritis and cachexia.
XX
PS   Disclosure; Page 160-162; 211pp; English.
XX
CC   The invention relates to a novel concatameric protein comprising two
CC   soluble domains, in which an N-terminus of a soluble domain of a
CC   biologically active protein is linked to a C-terminus of an identical
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CC   soluble domain or a different soluble domain of a biologically active
CC   protein. The methods and compositions of the present invention are useful
CC   for the diagnosis and treatment of disorders associated with dimeric
CC   protein or its glycosylated form, such as inflammation, septicaemia,
CC   cytotoxicity, rheumatoid arthritis, cachexia and other inflammation-
CC   related diseases. This polynucleotide sequence represents the DNA
CC   encoding a human concatameric protein of the invention
XX
SQ   Sequence 1134 BP; 273 A; 352 C; 298 G; 211 T; 0 U; 0 Other;

  Query Match             90.5%;  Score 695;  DB 8;  Length 1134;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-137;
  Matches  695;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 GCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTC 64
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        433 GCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTC 492

Qy         65 CTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCC 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        493 CTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCC 552

Qy        125 CGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAG 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        553 CGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAG 612

Qy        185 TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAG 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        613 TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAG 672

Qy        245 CAGTACAACAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        673 CAGTACAACAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG 732

Qy        305 AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAA 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        733 AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAA 792

Qy        365 ACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCC 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        793 ACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCC 852

Qy        425 CGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        853 CGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC 912

Qy        485 AGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACG 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        913 AGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACG 972

Qy        545 CCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAG 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        973 CCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAG 1032

Qy        605 AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAC 664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1033 AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAC 1092

Qy        665 CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG 699
              |||||||||||||||||||||||||||||||||||
Db       1093 CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG 1127


RESULT 12
ADQ79913
ID   ADQ79913 standard; DNA; 1134 BP.
XX
AC   ADQ79913;
XX
DT   09-SEP-2004  (first entry)
XX
DE   Human CTLA4/Ig construct DNA.
XX
KW   Human; tumour necrosis factor receptor; TNFR1; TNFR2; CTLA4; CD2; IgG;
KW   immunoglobulin; ds; concatameric fused dimer protein; immunoadhesin;
KW   Fc fragment; hinge.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   KR2004009997-A.
XX
PD   31-JAN-2004.
XX
PF   26-JUL-2002; 2002KR-00045921.
XX
PR   26-JUL-2002; 2002KR-00045921.
XX
PA   (MEDE-) MEDEXGEN INC.
XX
PI   Choi EY,  Han JU,  Jung YH,  Kim JM,  Lee HJ;
XX
DR   WPI; 2004-458871/43.
DR   P-PSDB; ADQ79914.
XX
PT   Concatameric immunoadhesin.
XX
PS   Example 2; SEQ ID NO 15; 129pp; Korean.
XX
CC   The invention relates to a concatameric fused dimer protein and
CC   glycosylation modification protein providing concatameric immunoadhesin
CC   with improved efficacy and stability. The concatameric protein is
CC   characteristically formed by binding C-terminal of one biologically
CC   active protein with N-terminal of same or different biologically active
CC   protein, e.g. tumour necrosis factor receptors (TNFR1 and TNFR2), CD2 and
CC   CTLA4. Two monomer proteins which are formed by fusing the extracellular
CC   region of a protein participating in the same immune reaction to an
CC   immunoglobulin Fc fragment, bound together at a hinge region by
CC   disulphide bond to give the concatameric fused dimer protein, wherein the
CC   immunoglobulin is IgG. The present sequence encodes a monomeric or
CC   dimeric IgG fusion protein (or a dimeric fusion protein containing
CC   engineered N-glycosylation sites, designated "mg").
XX
SQ   Sequence 1134 BP; 273 A; 352 C; 298 G; 211 T; 0 U; 0 Other;

  Query Match             90.5%;  Score 695;  DB 12;  Length 1134;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-137;
  Matches  695;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 GCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTC 64
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        433 GCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTC 492

Qy         65 CTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCC 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        493 CTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCC 552

Qy        125 CGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAG 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        553 CGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAG 612

Qy        185 TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAG 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        613 TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAG 672

Qy        245 CAGTACAACAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        673 CAGTACAACAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG 732

Qy        305 AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAA 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        733 AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAA 792

Qy        365 ACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCC 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        793 ACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCC 852
```

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Qy        425 CGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        853 CGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC 912

Qy        485 AGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACG 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        913 AGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACG 972

Qy        545 CCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAG 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        973 CCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAG 1032

Qy        605 AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAC 664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1033 AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAC 1092

Qy        665 CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG 699
              |||||||||||||||||||||||||||||||||||
Db       1093 CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG 1127
```

RESULT 13
ABT32047
ID ABT32047 standard; DNA; 1314 BP.
XX
AC ABT32047;
XX
DT 08-MAY-2003 (first entry)
XX
DE Concatameric immunoadhesion human DNA sequence SEQ ID No 13.
XX
KW Antiinflammatory; antibacterial; immunosuppressive; antirheumatic;
KW antiarthritic; immunomodulator; concatameric protein; soluble domain;
KW dimeric protein; inflammation; septicaemia; cytotoxicity;
KW rheumatoid arthritis; cachexia; inflammation; human; gene; ds.
XX
OS Homo sapiens.
XX
PN WO2003010202-A1.
XX
PD 06-FEB-2003.
XX
PF 26-JUL-2002; 2002WO-KR001427.
XX
PR 26-JUL-2001; 2001KR-00045028.
XX
PA (MEDE-) MEDEXGEN CO LTD.
XX
PI Chung Y, Han J, Lee H, Choi E, Kim J;
XX
DR WPI; 2003-229639/22.
DR P-PSDB; ABJ37104.
XX
PT New concatameric protein having two soluble domains, useful for
PT diagnosing and treating disorders associated with the dimeric protein or
PT its glycosylated form, such as inflammation, septicemia, rheumatoid
PT arthritis and cachexia.
XX
PS Disclosure; Page 153-156; 211pp; English.
XX
CC The invention relates to a novel concatameric protein comprising two
CC soluble domains, in which an N-terminus of a soluble domain of a
CC biologically active protein is linked to a C-terminus of an identical
CC soluble domain or a different soluble domain of a biologically active
CC protein. The methods and compositions of the present invention are useful
CC for the diagnosis and treatment of disorders associated with dimeric
CC protein or its glycosylated form, such as inflammation, septicaemia,
CC cytotoxicity, rheumatoid arthritis, cachexia and other inflammation-
CC related diseases. This polynucleotide sequence represents the DNA
CC encoding a human concatameric protein of the invention
XX
SQ Sequence 1314 BP; 400 A; 342 C; 312 G; 260 T; 0 U; 0 Other;

```
  Query Match             90.5%;  Score 695;  DB 8;  Length 1314;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-137;
  Matches  695;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 GCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTC 64
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        613 GCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTC 672

Qy         65 CTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCC 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        673 CTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCC 732

Qy        125 CGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAG 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        733 CGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAG 792

Qy        185 TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAG 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        793 TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAG 852

Qy        245 CAGTACAACAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        853 CAGTACAACAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG 912

Qy        305 AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAA 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        913 AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAA 972

Qy        365 ACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCC 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        973 ACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCC 1032

Qy        425 CGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1033 CGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC 1092

Qy        485 AGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACG 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1093 AGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACG 1152

Qy        545 CCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAG 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1153 CCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAG 1212

Qy        605 AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAC 664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1213 AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAC 1272

Qy        665 CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG 699
              |||||||||||||||||||||||||||||||||||
Db       1273 CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG 1307
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RESULT 14
ADQ79911
ID ADQ79911 standard; DNA; 1314 BP.
XX
AC ADQ79911;
XX
DT 09-SEP-2004 (first entry)
XX
DE Human CD2/Ig construct DNA.
XX
KW Human; tumour necrosis factor receptor; TNFR1; TNFR2; CTLA4; CD2; IgG;
KW immunoglobulin; ds; concatameric fused dimer protein; immunoadhesin;
KW Fc fragment; hinge.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN KR2004009997-A.
XX

PD 31-JAN-2004.
XX
PF 26-JUL-2002; 2002KR-00045921.
XX
PR 26-JUL-2002; 2002KR-00045921.
XX
PA (MEDE-) MEDEXGEN INC.
XX
PI Choi EY, Han JU, Jung YH, Kim JM, Lee HJ;
XX
DR WPI; 2004-458871/43.
DR P-PSDB; ADQ79912.
XX
PT Concatameric immunoadhesin.
XX
PS Example 2; SEQ ID NO 13; 129pp; Korean.
XX
CC The invention relates to a concatameric fused dimer protein and
CC glycosylation modification protein providing concatameric immunoadhesin
CC with improved efficacy and stability. The concatameric protein is
CC characteristically formed by binding C-terminal of one biologically
CC active protein with N-terminal of same or different biologically active
CC protein, e.g. tumour necrosis factor receptors (TNFR1 and TNFR2), CD2 and
CC CTLA4. Two monomer proteins which are formed by fusing the extracellular
CC region of a protein participating in the same immune reaction to an
CC immunoglobulin Fc fragment, bound together at a hinge region by
CC disulphide bond to give the concatameric fused dimer protein, wherein the
CC immunoglobulin is IgG. The present sequence encodes a monomeric or
CC dimeric IgG fusion protein (or a dimeric fusion protein containing
CC engineered N-glycosylation sites, designated "mg").
XX
SQ Sequence 1314 BP; 400 A; 342 C; 312 G; 260 T; 0 U; 0 Other;

Query Match 90.5%; Score 695; DB 12; Length 1314;
Best Local Similarity 100.0%; Pred. No. 1.6e-137;
Matches 695; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          5 GCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTC 64
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        613 GCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTC 672

Qy         65 CTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCC 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        673 CTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCC 732

Qy        125 CGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAG 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        733 CGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAG 792

Qy        185 TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAG 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        793 TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAG 852

Qy        245 CAGTACAACAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        853 CAGTACAACAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG 912

Qy        305 AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAA 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        913 AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAA 972

Qy        365 ACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCC 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        973 ACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCC 1032

Qy        425 CGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1033 CGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC 1092

Qy        485 AGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACG 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1093 AGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACG 1152

Qy        545 CCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAG 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1153 CCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAG 1212

Qy        605 AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAC 664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1213 AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAC 1272

Qy        665 CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG 699
              |||||||||||||||||||||||||||||||||||
Db       1273 CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG 1307
```

RESULT 15
ABT32046
ID ABT32046 standard; DNA; 1980 BP.
XX
AC ABT32046;
XX
DT 08-MAY-2003 (first entry)
XX
DE Concatameric immunoadhesion human DNA sequence SEQ ID No 11.
XX
KW Antiinflammatory; antibacterial; immunosuppressive; antirheumatic;
KW antiarthritic; immunomodulator; concatameric protein; soluble domain;
KW dimeric protein; inflammation; septicaemia; cytotoxicity;
KW rheumatoid arthritis; cachexia; inflammation; human; gene; ds.
XX
OS Homo sapiens.
XX
PN WO2003010202-A1.
XX
PD 06-FEB-2003.
XX
PF 26-JUL-2002; 2002WO-KR001427.
XX
PR 26-JUL-2001; 2001KR-00045028.
XX
PA (MEDE-) MEDEXGEN CO LTD.
XX
PI Chung Y, Han J, Lee H, Choi E, Kim J;
XX
DR WPI; 2003-229639/22.
DR P-PSDB; ABJ37103.
XX
PT New concatameric protein having two soluble domains, useful for
PT diagnosing and treating disorders associated with the dimeric protein or
PT its glycosylated form, such as inflammation, septicemia, rheumatoid
PT arthritis and cachexia.
XX
PS Claim 29; Page 144-148; 211pp; English.
XX
CC The invention relates to a novel concatameric protein comprising two
CC soluble domains, in which an N-terminus of a soluble domain of a
CC biologically active protein is linked to a C-terminus of an identical
CC soluble domain or a different soluble domain of a biologically active
CC protein. The methods and compositions of the present invention are useful
CC for the diagnosis and treatment of disorders associated with dimeric
CC protein or its glycosylated form, such as inflammation, septicaemia,
CC cytotoxicity, rheumatoid arthritis, cachexia and other inflammation-
CC related diseases. This polynucleotide sequence represents the DNA
CC encoding a human concatameric protein of the invention
XX
SQ Sequence 1980 BP; 443 A; 658 C; 554 G; 325 T; 0 U; 0 Other;

Query Match 90.5%; Score 695; DB 8; Length 1980;
Best Local Similarity 100.0%; Pred. No. 1.7e-137;
Matches 695; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          5 GCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTC 64
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1279 GCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTC 1338
```

```
Qy        65 CTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCC 124
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1339 CTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCC 1398

Qy       125 CGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAG 184
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1399 CGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAG 1458

Qy       185 TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAG 244
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1459 TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAG 1518

Qy       245 CAGTACAACAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG 304
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1519 CAGTACAACAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG 1578

Qy       305 AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAA 364
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1579 AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAA 1638

Qy       365 ACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCC 424
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1639 ACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCC 1698

Qy       425 CGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC 484
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1699 CGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC 1758

Qy       485 AGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACG 544
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1759 AGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACG 1818

Qy       545 CCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAG 604
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1819 CCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAG 1878

Qy       605 AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAC 664
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1879 AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAC 1938

Qy       665 CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG 699
             |||||||||||||||||||||||||||||||||||
Db      1939 CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG 1973
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Search completed: March 8, 2005, 07:08:24
Job time : 478 secs

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